CLAIMS

What is claimed is:

1. A method for detecting an alteration in a target nucleic acid suspected to be in a biological sample, the method comprising the steps of:

a) adding, to a biological sample suspected to contain a target nucleic acid, a plurality of single-stranded peptide nucleic acids that hybridize contiguously to a region of said target nucleic acid if said region is unaltered;

b) adding to said biological sample an agent that degrades single-stranded nucleic acids; and,

c) detecting an alteration in said target nucleic acid as the presence of a degradation product from steps a) and b) resulting from degradation within said region of said target nucleic acid.

2. The method of claim 1, wherein said alteration is a disease-associated mutation.

3. The method of claim 2, wherein said disease is cancer.

4. The method of claim 2, further comprising the step of determining the identity of said alteration in said target nucleic acid.

5. The method of claim 1, wherein at least one member of said plurality of single-stranded peptide nucleic acids comprises a detectable label.

6. The method of claim 1, wherein said target nucleic acid suspected of being in said biological sample comprises a detectable label.

7. The method of claim 5 or 6, wherein said detectable label is selected from the group consisting of a fluorescent tag, a radioactive isotope, and a molecular weight marker.

8. The method of claim 1, wherein each member of said plurality of single-stranded peptide nucleic acids is between about 8 and about 30 nucleotides long.

9. The method of claim 1, wherein each member of said plurality of single-stranded peptide nucleic acids has an approximately equivalent hybridization melting temperature.

10. The method of claim 1, wherein said target nucleic acid is bound to a solid support.

11. The method of claim 10, wherein the 5' end of said target nucleic acid is bound to said solid support.

12. The method of claim 10, wherein the 3' end of said target nucleic acid is bound to said solid support.

13. The method of claim 1, wherein said biological sample comprises a tissue or body fluid.

14. The method of claim 1, wherein said agent is an enzyme.

15. The method of claim 14, wherein said enzyme is selected from the group consisting of S1, MutY, MutS, and Mungbean nuclease.

16. The method of claim 1, wherein said agent is a chemical agent.

17. The method of claim 2, wherein said alteration is selected from the group consisting of nucleotide insertions, deletions, rearrangements, transitions, translations, transversions, and substitutions.

18. The method of claim 13, wherein said tissue or body fluid is selected from the group consisting of sputum, pancreatic fluid, bile, lymph, plasma, urine, cerebrospinal fluid, seminal fluid, saliva, breast nipple aspirate, pus, biopsy tissue, fetal cells, and amniotic fluid.

19. The method of claim 13, wherein said tissue or body fluid is a stool sample.

20. The method of claim 1, wherein said alteration is a single nucleotide polymorphism.

21. The method of claim 1, wherein said alteration is inherited.

22. The method of claim 1, wherein said alteration exists as a subpopulation in a heterogeneous sample.

23. A method for detecting an alteration in a target nucleic acid suspected to be in a biological sample, the method comprising the steps of:

a) adding, to a biological sample suspected to contain a target nucleic acid, a plurality of probes that hybridize to a region of said target nucleic acid such that a gap separates adjacent hybridized probes, if said region is unaltered;

b) adding to said biological sample an agent under conditions that degrade single-stranded nucleic acids larger than said gap size; and,

c) detecting an alteration in said target nucleic acid as the presence of a degradation product from steps a) and b) resulting from degradation within said single-stranded region of said target nucleic acid.

24. A method for detecting an alteration in a polymorphic target nucleic acid suspected to be in a biological sample, the method comprising the steps of:

a) adding, to a biological sample suspected to contain a polymorphic target nucleic acid, a plurality of probes, said plurality comprising a probe complementary to each polymorphic varient of said target nucleic acid, such that said probes hybridize contiguously to a region of said target nucleic acid if said region is unaltered;

b) adding to said biological sample an agent that degrades single-stranded nucleic acids; and,

c) detecting an alteration in said target nucleic acid as the presence of a degradation product from steps a) and b) resulting from degradation within said region of said target nucleic acid.